

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/700, 3/3A  
Source: 1Fw16  
Date Processed by STIC: 3/21/06

***ENTERED***



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/700,313A

DATE: 03/21/2006

TIME: 08:49:52

Input Set : A:\seq listing.app  
 Output Set: N:\CRF4\03212006\J700313A.raw

3 <110> APPLICANT: Combadiere et al.  
 5 <120> TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS AND  
 THERAPEUTIC  
 6 AGENTS FOR HIV INFECTION  
 8 <130> FILE REFERENCE: 66645-01  
 10 <140> CURRENT APPLICATION NUMBER: US 10/700,313A  
 11 <141> CURRENT FILING DATE: 2003-10-31  
 13 <150> PRIOR APPLICATION NUMBER: US 60/018,508  
 14 <151> PRIOR FILING DATE: 1996-05-28  
 16 <150> PRIOR APPLICATION NUMBER: 08/864,458  
 17 <151> PRIOR FILING DATE: 1997-05-28  
 19 <160> NUMBER OF SEQ ID NOS: 10  
 21 <170> SOFTWARE: PatentIn version 3.3  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 1225  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (27)...(1082)  
 33 <400> SEQUENCE: 1  
 34 aagaaaactct ccccggtgg aacaag atg gat tat caa gtg tca agt cca atc 53  
 35 Met Asp Tyr Gln Val Ser Ser Pro Ile  
 36 1 5  
 38 tat gac atc aat tat tat aca tcg gag ccc tgc caa aaa atc aat gtg 101  
 39 Tyr Asp Ile Asn Tyr Tyr Ser Glu Pro Cys Gln Lys Ile Asn Val  
 40 10 15 20 25  
 42 aag caa atc gca gcc cgc ctc ctg cct ccg ctc tac tca ctg gtg ttc 149  
 43 Lys Gln Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe  
 44 30 35 40  
 46 atc ttt ggt ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac 197  
 47 Ile Phe Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn  
 48 45 50 55  
 50 tgc aaa agg ctg aag agc atg act gac atc tac ctg ctc aac ctg gcc 245  
 51 Cys Lys Arg Leu Lys Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala  
 52 60 65 70  
 54 atc tct gac ctg ttt ttc ctt act gtc ccc ttc tgg gct cac tac 293  
 55 Ile Ser Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr  
 56 75 80 85  
 58 ttg gcc gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca 341  
 59 Leu Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr  
 60 90 95 100 105  
 62 ggg ctc tat ttt ata ggc ttc ttc tct gga atc ttc atc atc atc ctc 389  
 63 Gly Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu

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Input Set : A:\seq listing.app  
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64	110	115	120	
66	ctg aca atc gat agg tac ctg gct gtc gtc cat gct gtg ttt gct tta			437
67	Leu Thr Ile Asp Arg Tyr Leu Ala Val Val His Ala Val Phe Ala Leu			
68	125	130	135	
70	aaa gcc agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg			485
71	Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp			
72	140	145	150	
74	gtg gtg gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct			533
75	Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser			
76	155	160	165	
78	caa aaa gaa ggt ctt cat tac acc tgc agc tct cat ttt cca tac agt			581
79	Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser			
80	170	175	180	185
82	cag tat caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc tgg			629
83	Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu			
84	190	195	200	
86	ggg ctg gtc ctg ccg ctt gtc atg gtc atc tgc tac tcg gga atc			677
87	Gly Leu Val Leu Pro Leu Val Met Val Ile Cys Tyr Ser Gly Ile			
88	205	210	215	
90	cta aaa act ctg ctt cgg tgt cga aat gag aag aag agg cac agg gct			725
91	Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala			
92	220	225	230	
94	gtg agg ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct			773
95	Val Arg Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala			
96	235	240	245	
98	ccc tac aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc			821
99	Pro Tyr Asn Ile Val Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly			
100	250	255	260	265
102	ctg aat aat tgc agt agc tct aac agg ttg gac caa gct atg cag gtg			869
103	Leu Asn Asn Cys Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val			
104	270	275	280	
106	aca gag act ctt ggg atg acg cac tgc tgc atc aac ccc atc atc tat			917
107	Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr			
108	285	290	295	
110	gcc ttt gtc ggg gag aag ttc aga aac tac ctc tta gtc ttc ttc caa			965
111	Ala Phe Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln			
112	300	305	310	
114	aag cac att gcc aaa cgc ttc tgc aaa tgc tgt tct att ttc cag caa			1013
115	Lys His Ile Ala Lys Arg Phe Cys Lys Cys Ser Ile Phe Gln Gln			
116	315	320	325	
118	gag gct ccc gag cga gca agc tca gtt tac acc cga tcc act ggg gag			1061
119	Glu Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu			
120	330	335	340	345
122	cag gaa ata tct gtg ggc ttg tgacacggac tcaagtgggc tggtgaccga			1112
123	Gln Glu Ile Ser Val Gly Leu			
124	350			
126	gtcagagttg tgcacatggc ttagtttca tacacagcct gggctggggg tgggggtggga			1172
128	gaggtctttt ttaaaaaggaa gttactgtta tagagggtct aagattcatac cat			1225
131	<210> SEQ ID NO: 2			

RAW SEQUENCE LISTING  
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Input Set : A:\seq listing.app  
Output Set: N:\CRF4\03212006\J700313A.raw

132 <211> LENGTH: 352  
133 <212> TYPE: PRT  
134 <213> ORGANISM: Homo sapiens  
136 <400> SEQUENCE: 2  
138 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr  
139 1 5 10 15  
142 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu  
143 20 25 30  
146 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn  
147 35 40 45  
150 Met Leu Val Ile Leu Ile Ile Asn Cys Lys Arg Leu Lys Ser Met  
151 50 55 60  
154 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu  
155 65 70 75 80  
158 Leu Thr Val Pro Phe Trp Ala His Tyr Leu Ala Ala Gln Trp Asp Phe  
159 85 90 95  
162 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe  
163 100 105 110  
166 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu  
167 115 120 125  
170 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe  
171 130 135 140  
174 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser  
175 145 150 155 160  
178 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr  
179 165 170 175  
182 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn  
183 180 185 190  
186 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu  
187 195 200 205  
190 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys  
191 210 215 220  
194 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile  
195 225 230 235 240  
198 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu  
199 245 250 255  
202 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser  
203 260 265 270  
206 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr  
207 275 280 285  
210 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe  
211 290 295 300  
214 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe  
215 305 310 315 320  
218 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser  
219 325 330 335  
222 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu  
223 340 345 350  
226 <210> SEQ ID NO: 3

RAW SEQUENCE LISTING DATE: 03/21/2006  
PATENT APPLICATION: US/10/700,313A TIME: 08:49:52

Input Set : A:\seq listing.app  
Output Set: N:\CRF4\03212006\J700313A.raw

227 <211> LENGTH: 1225  
 228 <212> TYPE: DNA  
 229 <213> ORGANISM: Homo sapiens  
 232 <220> FEATURE:  
 233 <221> NAME/KEY: CDS  
 234 <222> LOCATION: (27)..(1082)  
 236 <400> SEQUENCE: 3

237	aagaaaactct	ccccgggtgg	aacaag	atg	gat	tat	caa	gtg	tca	agt	cca	atc	53				
238							Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile		
239							1			5							
241	tat	gac	atc	aat	tat	tat	aca	tcg	gag	ccc	tgc	caa	aaa	atc	aat	gtg	101
242	Tyr	Asp	Ile	Asn	Tyr	Tyr	Ser	Glu	Pro	Cys	Gln	Lys	Ile	Asn	Val		
243	10					15				20				25			
245	aag	caa	atc	gca	gcc	cgc	ctc	ctg	cct	ccg	ctc	tac	tca	ctg	gtg	ttc	149
246	Lys	Gln	Ile	Ala	Ala	Arg	Leu	Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	
247							30			35				40			
249	atc	ttt	ggt	ttt	gtg	ggc	aac	atg	ctg	gtc	atc	ctc	atc	ctg	ata	aac	197
250	Ile	Phe	Gly	Phe	Val	Gly	Asn	Met	Leu	Val	Ile	Leu	Ile	Leu	Ile	Asn	
251							45			50				55			
253	tgc	aaa	agg	ctg	aag	agc	atg	act	gac	atc	tac	ctg	ctc	aac	ctg	gcc	245
254	Cys	Lys	Arg	Leu	Lys	Ser	Met	Thr	Asp	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	
255							60			65				70			
257	atc	tct	gac	ctg	ttt	ttc	ctt	act	gtc	ccc	ttc	tgg	gct	cac	tat	293	
258	Ile	Ser	Asp	Leu	Phe	Phe	Leu	Leu	Thr	Val	Pro	Phe	Trp	Ala	His	Tyr	
259							75			80				85			
261	gct	gcc	gcc	cag	tgg	gac	ttt	gga	aat	aca	atg	tgt	caa	ctc	ttg	aca	341
262	Ala	Ala	Ala	Gln	Trp	Asp	Phe	Gly	Asn	Thr	Met	Cys	Gln	Leu	Leu	Thr	
263							90			95				100		105	
265	ggg	ctc	tat	ttt	ata	ggc	ttc	ttc	tct	gga	atc	ttc	ttc	atc	atc	ctc	389
266	Gly	Leu	Tyr	Phe	Ile	Gly	Phe	Phe	Ser	Gly	Ile	Phe	Phe	Ile	Ile	Leu	
267							110				115				120		
269	ctg	aca	atc	gat	agg	tac	ctg	gct	gtc	gtc	cat	gct	gtg	ttt	gct	tta	437
270	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	Ala	Val	Val	His	Ala	Val	Phe	Ala	Leu	
271							125			130				135			
273	aaa	gcc	agg	acg	gtc	acc	ttt	ggg	gtg	gtg	aca	agt	gtg	atc	act	tgg	485
274	Lys	Ala	Arg	Thr	Val	Thr	Phe	Gly	Val	Val	Thr	Ser	Val	Ile	Thr	Trp	
275							140			145				150			
277	gtg	gtg	gct	gtg	ttt	gcg	tct	ctc	cca	gga	atc	atc	ttt	acc	aga	tct	533
278	Val	Val	Ala	Val	Phe	Ala	Ser	Leu	Pro	Gly	Ile	Ile	Phe	Thr	Arg	Ser	
279							155			160				165			
281	caa	aaa	gaa	ggt	ctt	cat	tac	acc	tgc	agc	tct	cat	ttt	cca	tac	agt	581
282	Gln	Lys	Glu	Gly	Leu	His	Tyr	Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	
283							170			175				180		185	
285	cag	tat	caa	ttc	tgg	aag	aat	ttc	cag	aca	tta	aag	ata	gtc	atc	ttg	629
286	Gln	Tyr	Gln	Phe	Trp	Lys	Asn	Phe	Gln	Thr	Leu	Lys	Ile	Val	Ile	Leu	
287							190				195				200		
289	ggg	ctg	gtc	ctg	ccg	ctg	ctt	gtc	atg	gtc	atc	tgc	tac	tcg	gga	atc	677
290	Gly	Leu	Val	Leu	Pro	Leu	Leu	Val	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	
291							205			210				215			

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293 cta aaa act ctg ctt cggttgt cga aat gag aag aag agg cac agg gct	725
294 Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala	
295 220 225 230	
297 gtg agg ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct	773
298 Val Arg Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala	
299 235 240 245	
301 ccc tac aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc	821
302 Pro Tyr Asn Ile Val Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly	
303 250 255 260 265	
305 ctg aat aat tgc agt agc tct aac agg ttg gac caa gct atg cag gtg	869
306 Leu Asn Asn Cys Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val	
307 270 275 280	
309 aca gag act ctt ggg atg acg cac tgc tgc atc aac ccc atc atc tat	917
310 Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr	
311 285 290 295	
313 gcc ttt gtc ggg gag aag ttc aga aac tac ctc tta gtc ttc ttc caa	965
314 Ala Phe Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln	
315 300 305 310	
317 aag cac att gcc aaa cgc ttc tgc aaa tgc tgt tct att ttc cag caa	1013
318 Lys His Ile Ala Lys Arg Phe Cys Lys Cys Ser Ile Phe Gln Gln	
319 315 320 325	
321 gag gct ccc gag cga gca agc tca gtt tac acc cga tcc act ggg gag	1061
322 Glu Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu	
323 330 335 340 345	
325 cag gaa ata tct gtg ggc ttg tgacacggac tcaagtgggc tggtgaccac	1112
326 Gln Glu Ile Ser Val Gly Leu	
327 350	
329 gtcagagttg tgcacatggc ttagtttca tacacagcct gggctggggg tgggggtggga	1172
331 gaggtcttt taaaaaggaa gttactgtta tagagggtct aagattcatc cat	1225
334 <210> SEQ ID NO: 4	
335 <211> LENGTH: 352	
336 <212> TYPE: PRT	
337 <213> ORGANISM: Homo sapiens	
339 <400> SEQUENCE: 4	
341 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr	
342 1 5 10 15	
345 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu	
346 20 25 30	
349 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn	
350 35 40 45	
353 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met	
354 50 55 60	
357 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu	
358 65 70 75 80	
361 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe	
362 85 90 95	
365 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe	
366 100 105 110	
369 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu	

RAW SEQUENCE LISTING ERROR SUMMARY                   DATE: 03/21/2006  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 1

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:10

**VERIFICATION SUMMARY**

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L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0